

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

5 (A) NAME: Vlaams Interuniversitair Instituut voor
Biotechnologie
(B) STREET: Rijvisschestraat 120
(C) CITY: Zwijnaarde
(E) COUNTRY: Belgium
10 (F) POSTAL CODE (ZIP): 9052B
(G) TELEPHONE: +32 9 2446611
(H) TELEFAX: +32 9 2446610

(ii) TITLE OF INVENTION: CD40 interacting and TRAF interacting proteins

15 (iii) NUMBER OF SEQUENCES: 6

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 1920 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 20..1108

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

| | | | | | | |
|---------------|------------|------------|------------|------------|-------------|-----|
| GTGCAGAGGC | GGCAGGAAGA | TGGAGTTGGG | GAGTTGCCTG | GAGGGCGGGA | GGGAGGCGGC | 60 |
| GGAGGAAGAG | GGCGAGCCTG | AGGTGAAAAA | GCGGCGACTT | CTGTGTGTGG | AGTTTGCCTC | 120 |
| GGTCGCAAGC | TGCGATGCCG | CAGTGGCTCA | GTGCTTCCTG | GCCGAGAACG | ACTGGGAGAT | 180 |
| GGAAAGGGCT | CTGAACTCCT | ACTTCGAGCC | TCCGGTGGAG | GAGAGCGCCT | TGGAACGCCG | 240 |
| 40 ACCTGAAACC | ATCTCTGAGC | CCAAGACCTA | TGTTGACCTA | ACCAATGAAG | AAACAACCTGA | 300 |
| TTCCACCACT | TCTAAAATCA | GCCCATCTGA | AGATACTCAG | CAAGAAAATG | GCAGCATGTT | 360 |
| CTCTCTCATT | ACCTGGAATA | TTGATGGATT | AGATCTAAAC | AATCTGTCAG | AGAGGGCTCG | 420 |

| | | | | | | | | |
|----|------------|-------------|-------------|------------|-------------|------------|-----------|------|
| | AGGGGTGTGT | TCC | TAG | CTTTGTACAG | CCCAGATGTG | ATATTTCT | GGAAGTTAT | 480 |
| | TCCCCCATAT | TATAGCTACC | TAAAGAAGAG | ATCAAGTAAT | TATGAGATTA | TTACAGGTCA | | 540 |
| | TGAAGAAGGA | TATTTACACAG | CTATAATGTT | GAAGAAATCA | AGAGTGAAAT | TAAAAAGCCA | | 600 |
| | AGAGATTATT | CCTTTTCCAA | GTACCAAAAT | GATGAGAAAC | CTTTTATGTG | TGCATGTGAA | | 660 |
| 5 | TGTGTCAGGA | AATGAGCTTT | GCCTTATGAC | ATCCCATTG | GAGAGCACCA | GAGGGCATGC | | 720 |
| | TGCGGAACGA | ATGAATCAGT | TAAAAATGGT | TTTAAAGAAA | ATGCAAGAGG | CTCCAGAGTC | | 780 |
| | AGCTACAGTT | ATATTTGCAG | GAGATACAAA | TCTAAGGGAT | CGAGAGGTTA | CCAGATGTGG | | 840 |
| | TGGTTTACCC | AACAACATTG | TGGATGTCTG | GGAGTTTTTG | GGCAAACCTA | AACATTGCCA | | 900 |
| | GTATACATGG | GATACACAAA | TGAACTCTAA | TCTTGGAATA | ACTGCTGCTT | GTAAACTTCG | | 960 |
| 10 | TTTTGATCGA | ATATTTTCA | GAGCAGCAGC | AGAAGAGGGA | CACATTATTC | CCCGAAGTTT | | 1020 |
| | GGACCTTCTT | GGATTAGAAA | AACTGGACTG | TGGTAGATTT | CCTAGTGATC | ACTGGGGTCT | | 1080 |
| | TCTGTGCAAC | TTAGATATAA | TATTGTAAAA | TGCTTTTCAA | GTGTGGGTTT | TGCCCTGATT | | 1140 |
| | GTTGCAAATA | CAATTTCCAC | CTTCTGGAAA | GGTAGGTTTG | CTGTGGAGGA | AATAATGTAC | | 1200 |
| | TAGATCATTG | TCACAGAAAA | ACCAACTATG | ATTTATGGTT | GTGTTTTTCAG | AATTCAACAT | | 1260 |
| 15 | TAAAGATTAA | TGTTTATTTA | AACGAACACA | TTCCTGCATT | CAGGATGTGA | GGCCATTTAA | | 1320 |
| | TAAAAAGGGC | ACAAAGCCTG | TCAGAGTTTT | CAACGGTGCT | TACAGCTGCC | AGCTGGATTC | | 1380 |
| | CAAACAGGTA | CCCCATTGTC | TCTGAGCTAA | TGTTTATATT | TTTCCATTCA | GGCACCGAAA | | 1440 |
| | TAGTTAATAT | TTAAAATAAG | TCTTCAAAAG | AAACATAAG | AGATTATTGA | GTTCTTGGA | | 1500 |
| | CTGGATCCTT | TATTTCATAA | GTTTCAATCA | TCTTAAATGA | AAATGCCATG | ATTATCTGCA | | 1560 |
| 20 | GTAAAGTAGA | TGACAGCTAT | TCTACATCAG | ACTTGATTTT | TGTCAGCTAA | TTACATAATT | | 1620 |
| | GGTAAGNTAT | AATTGAAACC | TTATGGCTTA | AAATTCCTTA | ACTCCTTTTT | GATTCATGTT | | 1680 |
| | TGTAGTCATG | TTGTCAACAG | AGGCAAAGTT | AAGCTTGATG | ATGGTTAAAA | TCGGTTTGAT | | 1740 |
| | AGCACCATGG | GACATTTTTT | TAACAAAAAT | AAATGCATGA | AGAGACATAG | CCTTTTAGTT | | 1800 |
| | TTGCTAATTG | TGAAATGGAA | ATGCTTTTACA | GGAAGTAAAT | GCAAATTANT | TTTAAGTGTG | | 1860 |
| 25 | CTTTAAAGAA | AAATATTTTC | CCCACAGGAG | AAATTTAAAT | AAAGAATTTT | ATTTGGTAAA | | 1920 |

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

5 Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu
1 5 10 15
Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe
20 25 30
Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala
35 40 45
10 Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
50 55 60
Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu
65 70 75 80
15 Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr
85 90 95
Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser
100 105 110
Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn
115 120 125
20 Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser
130 135 140
Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr
145 150 155 160
25 Leu Lys Lys Arg Ser Ser Asn Tyr Glu Ile Ile Thr Gly His Glu Glu
165 170 175
Gly Tyr Phe Thr Ala Ile Met Leu Lys Lys Ser Arg Val Lys Leu Lys
180 185 190
Ser Gln Glu Ile Ile Pro Phe Pro Ser Thr Lys Met Met Arg Asn Leu
195 200 205
30 Leu Cys Val His Val Asn Val Ser Gly Asn Glu Leu Cys Leu Met Thr
210 215 220
Ser His Leu Glu Ser Thr Arg Gly His Ala Ala Glu Arg Met Asn Gln
225 230 235 240
35 Leu Lys Met Val Leu Lys Lys Met Gln Glu Ala Pro Glu Ser Ala Thr
245 250 255
Val Ile Phe Ala Gly Asp Thr Asn Leu Arg Asp Arg Glu Val Thr Arg
260 265 270
Cys Gly Gly Leu Pro Asn Asn Ile Val Asp Val Trp Glu Phe Leu Gly
275 280 285
40 Lys Pro Lys His Cys Gln Tyr Thr Trp Asp Thr Gln Met Asn Ser Asn
290 295 300
Leu Gly Ile Thr Ala Ala Cys Lys Leu Arg Phe Asp Arg Ile Phe Phe

305 310 315 320
 Arg Ala Ala Ala Glu Glu Gly His Ile Ile Pro Arg Ser Leu Asp Leu
 325 330 335
 Leu Gly Leu Glu Lys Leu Asp Cys Gly Arg Phe Pro Ser Asp His Trp
 5 340 345 350
 Gly Leu Leu Cys Asn Leu Asp Ile Ile Leu
 355 360

(2) INFORMATION FOR SEQ ID NO: 3:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mus musculus

20 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:122..1234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

| | | |
|----|--|-----|
| | AGCTATTAAT GATTCGAATT TATACGACTC ACTATAGGGA ATTTGGCCCT CGAGGCCAAG | 60 |
| | AATTCGGCAC GAGGGCGGGA AGCAGCGTGA AGAGCGGGTG TTTTGAGGGG ACCCTGCGGC | 120 |
| 25 | G ATG GCG TCT GGC AGC AGT TCC GAT GCG GCG GAG CCC GCA GGG CCG Met Ala Ser Gly Ser Ser Ser Asp Ala Ala Glu Pro Ala Gly Pro | 166 |
| | 1 5 10 15 | |
| | GCA GGG CGG GCG GCG TCG GCG CCC GAA GCA GCA CAG GCG GAG GAG GAC | 214 |
| 30 | Ala Gly Arg Ala Ala Ser Ala Pro Glu Ala Ala Gln Ala Glu Glu Asp | |
| | 20 25 30 | |
| | CGG GTG AAG AGG CGG CGG CTT CAG TGC CTG GGC TTT GCG TTG GTG GGG | 262 |
| | Arg Val Lys Arg Arg Arg Leu Gln Cys Leu Gly Phe Ala Leu Val Gly | |
| | 35 40 45 | |
| | GGA TGC GAC CCC ACG ATG GTC CCC AGC GTC CTG CGG GAG AAC GAC TGG | 310 |
| 35 | Gly Cys Asp Pro Thr Met Val Pro Ser Val Leu Arg Glu Asn Asp Trp | |
| | 50 55 60 | |
| | CAG ACG CAG AAA GCC CTG AGC GCC TAC TTC GAG CTG CCA GAG AAC GAC | 358 |
| | Gln Thr Gln Lys Ala Leu Ser Ala Tyr Phe Glu Leu Pro Glu Asn Asp | |
| | 65 70 75 | |
| 40 | CAA GGG TGG CCG CGC CAG CCT CCC ACG TCC TTC AAG TCC GAG GCC TAT | 406 |
| | Gln Gly Trp Pro Arg Gln Pro Pro Thr Ser Phe Lys Ser Glu Ala Tyr | |
| | 80 85 90 95 | |
| | GTT GAT CTA ACC AAC GAG GAT GCA AAT GAT ACA ACC ATT TTA GAA GCC | 454 |
| | Val Asp Leu Thr Asn Glu Asp Ala Asn Asp Thr Thr Ile Leu Glu Ala | |

| | 0 | | | | | | 105 | | | | | | 110 | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|--|
| | AGT | CCA | TCT | GGA | ACT | CCT | CTA | GAA | GAT | AGC | AGC | ACT | ATT | TCT | TTC | ATT | 502 | | |
| | Ser | Pro | Ser | Gly | Thr | Pro | Leu | Glu | Asp | Ser | Ser | Thr | Ile | Ser | Phe | Ile | | | |
| | | | | 115 | | | | | 120 | | | | | 125 | | | | | |
| 5 | ACC | TGG | AAT | ATT | GAT | GGA | TTA | GAT | GGA | TGC | AAT | CTG | CCC | GAG | AGG | GCT | 550 | | |
| | Thr | Trp | Asn | Ile | Asp | Gly | Leu | Asp | Gly | Cys | Asn | Leu | Pro | Glu | Arg | Ala | | | |
| | | | 130 | | | | | 135 | | | | | 140 | | | | | | |
| | CGA | GGG | GTG | TGT | TCC | TGC | CTA | GCT | TTG | TAT | AGT | CCA | GAT | GTG | GTA | TTT | 598 | | |
| 10 | Arg | Gly | Val | Cys | Ser | Cys | Leu | Ala | Leu | Tyr | Ser | Pro | Asp | Val | Val | Phe | | | |
| | | 145 | | | | | 150 | | | | | 155 | | | | | | | |
| | CTA | CAG | GAA | GTT | ATC | CCC | CCA | TAC | TGT | GCC | TAC | CTA | AAG | AAG | AGA | GCA | 646 | | |
| | Leu | Gln | Glu | Val | Ile | Pro | Pro | Tyr | Cys | Ala | Tyr | Leu | Lys | Lys | Arg | Ala | | | |
| | 160 | | | | | 165 | | | | 170 | | | | | | 175 | | | |
| 15 | GCC | AGT | TAC | ACA | ATT | ATT | ACA | GGT | AAT | GAA | GAA | GGA | TAT | TTC | ACA | GCT | 694 | | |
| | Ala | Ser | Tyr | Thr | Ile | Ile | Thr | Gly | Asn | Glu | Glu | Gly | Tyr | Phe | Thr | Ala | | | |
| | | | | 180 | | | | 185 | | | | | | 190 | | | | | |
| | ATA | CTA | TTG | AAG | AAA | GGA | AGA | GTG | AAA | TTT | AAA | AGT | CAG | GAG | ATT | ATT | 742 | | |
| | Ile | Leu | Leu | Lys | Lys | Gly | Arg | Val | Lys | Phe | Lys | Ser | Gln | Glu | Ile | Ile | | | |
| | | | 195 | | | | | 200 | | | | | | 205 | | | | | |
| 20 | CCT | TTT | CCA | AAT | ACC | AAA | ATG | ATG | AGA | AAC | CTG | CTA | TGC | GTA | AAT | GTG | 790 | | |
| | Pro | Phe | Pro | Asn | Thr | Lys | Met | Met | Arg | Asn | Leu | Leu | Cys | Val | Asn | Val | | | |
| | | | 210 | | | | 215 | | | | | | 220 | | | | | | |
| | AGT | TTG | GGT | GGA | AAT | GAA | TTT | TGC | CTT | ATG | ACA | TCC | CAT | TTG | GAG | AGC | 838 | | |
| 25 | Ser | Leu | Gly | Gly | Asn | Glu | Phe | Cys | Leu | Met | Thr | Ser | His | Leu | Glu | Ser | | | |
| | | 225 | | | | | 230 | | | | | 235 | | | | | | | |
| | ACC | AGA | GAA | CAT | TCT | GCG | GAA | CGA | ATA | AGA | CAA | TTA | AAA | ACT | GTT | CTT | 886 | | |
| | Thr | Arg | Glu | His | Ser | Ala | Glu | Arg | Ile | Arg | Gln | Leu | Lys | Thr | Val | Leu | | | |
| | 240 | | | | | 245 | | | | | 250 | | | | | 255 | | | |
| 30 | GGA | AAA | ATG | CAA | GAG | GCT | CCA | GAT | TCA | ACC | ACG | GTT | ATA | TTT | GCA | GGA | 934 | | |
| | Gly | Lys | Met | Gln | Glu | Ala | Pro | Asp | Ser | Thr | Thr | Val | Ile | Phe | Ala | Gly | | | |
| | | | | 260 | | | | 265 | | | | | | 270 | | | | | |
| | GAT | ACA | AAT | TTA | AGA | GAT | CAA | GAA | GTT | ATC | AAA | TGT | GGT | GGT | TTA | CCT | 982 | | |
| | Asp | Thr | Asn | Leu | Arg | Asp | Gln | Glu | Val | Ile | Lys | Cys | Gly | Gly | Leu | Pro | | | |
| | | | | 275 | | | | 280 | | | | | | 285 | | | | | |
| 35 | GAC | AAC | GTT | TTT | GAT | GCC | TGG | GAA | TTT | TTA | GGC | AAA | CCT | AAA | CAT | TGC | 1030 | | |
| | Asp | Asn | Val | Phe | Asp | Ala | Trp | Glu | Phe | Leu | Gly | Lys | Pro | Lys | His | Cys | | | |
| | | | 290 | | | | 295 | | | | | 300 | | | | | | | |
| | CAG | TAT | ACA | TGG | GAT | ACG | AAA | GCA | AAT | AAC | AAC | CTC | AGG | ATC | CCT | GCT | 1078 | | |
| 40 | Gln | Tyr | Thr | Trp | Asp | Thr | Lys | Ala | Asn | Asn | Asn | Leu | Arg | Ile | Pro | Ala | | | |
| | | 305 | | | | | 310 | | | | | 315 | | | | | | | |
| | GCT | TAT | AAG | CAT | CGT | TTT | GAT | CGA | ATA | TTT | TTC | AGA | GCA | GAA | GAG | GGG | 1126 | | |
| | Ala | Tyr | Lys | His | Arg | Phe | Asp | Arg | Ile | Phe | Phe | Arg | Ala | Glu | Glu | Gly | | | |
| | 320 | | | | | 325 | | | | | 330 | | | | | 335 | | | |
| 45 | CAC | CTT | ATT | CCT | CAA | AGT | TTA | GAC | CTT | GTT | GGG | TTG | GAA | AAA | CTG | GAC | 1174 | | |
| | His | Leu | Ile | Pro | Gln | Ser | Leu | Asp | Leu | Val | Gly | Leu | Glu | Lys | Leu | Asp | | | |
| | | | | 340 | | | | 345 | | | | | | | 350 | | | | |
| | TGT | GGT | AGA | TTT | CCG | AGT | GAT | CAC | TGG | GGG | CTC | TTG | TGC | ACC | TTG | AAT | 1222 | | |
| | Cys | Gly | Arg | Phe | Pro | Ser | Asp | His | Trp | Gly | Leu | Leu | Cys | Thr | Leu | Asn | | | |
| | | | | 355 | | | | 360 | | | | | | 365 | | | | | |

GTA GTA TTG TG AGCTTCCC ACTTGCAGCT TTACACGTTT GTT CTA
 Val Val Leu *
 370

1274

GTTCTGAATT TGTGTAGGTC TCAACCTTTC AGGACATC

1312

5 (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Ser Gly Ser Ser Ser Asp Ala Ala Glu Pro Ala Gly Pro Ala
 1 5 10 15
 Gly Arg Ala Ala Ser Ala Pro Glu Ala Ala Gln Ala Glu Glu Asp Arg
 15 20 25 30
 Val Lys Arg Arg Arg Leu Gln Cys Leu Gly Phe Ala Leu Val Gly Gly
 35 40 45
 Cys Asp Pro Thr Met Val Pro Ser Val Leu Arg Glu Asn Asp Trp Gln
 50 55 60
 20 Thr Gln Lys Ala Leu Ser Ala Tyr Phe Glu Leu Pro Glu Asn Asp Gln
 65 70 75 80
 Gly Trp Pro Arg Gln Pro Pro Thr Ser Phe Lys Ser Glu Ala Tyr Val
 85 90 95
 Asp Leu Thr Asn Glu Asp Ala Asn Asp Thr Thr Ile Leu Glu Ala Ser
 100 105 110
 25 Pro Ser Gly Thr Pro Leu Glu Asp Ser Ser Thr Ile Ser Phe Ile Thr
 115 120 125
 Trp Asn Ile Asp Gly Leu Asp Gly Cys Asn Leu Pro Glu Arg Ala Arg
 130 135 140
 30 Gly Val Cys Ser Cys Leu Ala Leu Tyr Ser Pro Asp Val Val Phe Leu
 145 150 155 160
 Gln Glu Val Ile Pro Pro Tyr Cys Ala Tyr Leu Lys Lys Arg Ala Ala
 165 170 175
 Ser Tyr Thr Ile Ile Thr Gly Asn Glu Glu Gly Tyr Phe Thr Ala Ile
 180 185 190
 35 Leu Leu Lys Lys Gly Arg Val Lys Phe Lys Ser Gln Glu Ile Ile Pro
 195 200 205
 Phe Pro Asn Thr Lys Met Met Arg Asn Leu Leu Cys Val Asn Val Ser
 210 215 220
 40 Leu Gly Gly Asn Glu Phe Cys Leu Met Thr Ser His Leu Glu Ser Thr
 225 230 235 240
 Arg Glu His Ser Ala Glu Arg Ile Arg Gln Leu Lys Thr Val Leu Gly
 245 250 255

Lys Met Gln Glu Ala Pro Asp Ser Thr Thr Val Ile Phe Gly Asp
 260 265
 Thr Asn Leu Arg Asp Gln Glu Val Ile Lys Cys Gly Gly Leu Pro Asp
 275 280 285
 5 Asn Val Phe Asp Ala Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln
 290 295 300
 Tyr Thr Trp Asp Thr Lys Ala Asn Asn Asn Leu Arg Ile Pro Ala Ala
 305 310 315 320
 10 Tyr Lys His Arg Phe Asp Arg Ile Phe Phe Arg Ala Glu Glu Gly His
 325 330 335
 Leu Ile Pro Gln Ser Leu Asp Leu Val Gly Leu Glu Lys Leu Asp Cys
 340 345 350
 Gly Arg Phe Pro Ser Asp His Trp Gly Leu Leu Cys Thr Leu Asn Val
 355 360 365
 15 Val Leu *
 370

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

25 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 209..1536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AGAGAAAGAG GCTCCGGGGA GATAGCGGAC CAGTGAGGGC TGCCCCTCTT TTGAAGCGGT 60
 TTTCGTCTCT TTCCGCCAGT GGCCTCCCAG CTCACGCAGG GGCGGGTCCC GGTAGCGCGA 120
 GGCGGTGCAG GGCGGGAAGG GGAGTGGTGG CGGCTGCGGC AGTAGGGACA GCAGGAGCAG 180
 35 TGGTGCTGTC AGCGCGGCCG TCGGAGACAT GGGAGACCCG GGGTCGGAAA TAATAGAATC 240
 TGTCCCTCCA GCTGGCCCTG AGGCATCTGA GTCAACAACG GATGAAAATG AAGACGACAT 300
 TCAGTTTGTC AGTGAAGGAC CATCGAGACC TGTCTTGAA TACATCGATC TGGTCTGTGG 360
 TGATGATGAA AACCCTAGCG CCTATTATAG TGATATTCTG TTTCTAAAA TGCCAAAACG 420
 ACAGGGTGAT TTTTGCATT TTTTAAATAT GAAGAAGGTG AAAACAGACA CAGAAAATAA 480
 40 TGAAGTGAGC AAAAATCACT GCAGATTGTC TAAGGCAAAG GAACCACATT TCGAGTATAT 540

AGAACAACCA ATC AAG AAAAGCCATC ACTTTCATCA AAGAAAGA TAGATAATCT 600
TGTGCTTCCA GATTGTTGGA ATGAAAAACA AGCATTATG TTTACAGAAC AATACAAATG 660
GCTTGAAATA AAAGAAGGTA AATTAGGATG TAAGGATTGT TCAGCAGTTC GGCATTGTTGG 720
ATCGAAAGCA GAAAAGCATG TCCATGTGTC CAAGGAATGG ATTGCATATT TAGTAACCCC 780
5 TAATGGCAGT AATAAACTA CTAGGCAAGC TTCTCTACGA AAAAAATTA GGGAACATGA 840
TGTTTCTAAA GCCCATGGTA AAATTCAGGA TTTGTTAAAG GAATCAACTA ATGATTCAAT 900
TTGTAATTTA GTGCATAAAC AAAATAATAA AAATATTGAT GCTACTGTAA AAGTTTTCAA 960
TACTGTTTAC AGTTTAGTAA AACATAACAG ACCTTTATCT GATATTGAGG GGGCAAGAGA 1020
ATTACAGGAA AAAAATGGAG AGGTAAATTG TTAAATACA CGTTACAGTG CAACAAGAAT 1080
10 AGCAGAACAT ATTGCAAAAG AAATGAAGAT GAAGATATTT AAGAATATTA TAGAAGAGAA 1140
TGCCAAAATC TGTATCATAA TTGATGAGGC ATCTACAGTT TCAAAGAAA CCACCCTAGT 1200
GATTTATCTC CAGTGCACAA TTCAGTCAGC TCCTGCACCT GTTATGTTAT TTGTGGCTTT 1260
AAAAGAATTG GTGTCAACTA TAGCAGAGTG TATTGTCAAT ACATTATTGA CTACTTTAAA 1320
TGATTGTGGT TTTACAAATG AATATTTGAA AGCAAATTTA ATTGCATTTT GTTCTGATGG 1380
15 TGCTAATACA ANCCTGGGAA GAAAGTCTGG AGTAGCTACA AAATTGTTAG AAAATTTTCC 1440
TGAAATCATC ATTTGGAAC TTTTAAATCA TCGATTACAA TTGTCATTG ATGATTCTAT 1500
ATCCGAAATA AAACAAATTA ATCATTTAAN NTATAA 1536

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 442 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

30 Met Gly Asp Pro Gly Ser Glu Ile Ile Glu Ser Val Pro Pro Ala Gly
1 5 10 15
Pro Glu Ala Ser Glu Ser Thr Thr Asp Glu Asn Glu Asp Asp Ile Gln
20 25 30
35 Phe Val Ser Glu Gly Pro Ser Arg Pro Val Leu Glu Tyr Ile Asp Leu
35 40 45
Val Cys Gly Asp Asp Glu Asn Pro Ser Ala Tyr Tyr Ser Asp Ile Leu

| | 50 | 55 | 6 |
|----|---|---|----------------------------|
| | Phe 65 | Pro Lys Met Pro Lys Arg Gln Gly Asp Phe 75 | Leu His Phe Leu Asn 80 |
| 5 | Met Lys Lys Val Lys 85 | Thr Asp Thr Glu Asn 90 | Asn Glu Val Ser Lys Asn 95 |
| | His Cys Arg Leu 100 | Ser Lys Ala Lys Glu Pro His Phe Glu Tyr Ile Glu 110 | |
| | Gln Pro Ile Ile Glu Glu Lys 115 | Pro Ser Leu Ser Ser Lys Lys Glu Ile 125 | |
| 10 | Asp Asn Leu Val Leu Pro Asp 130 | Cys Trp Asn Glu Lys Gln Ala Phe Met 140 | |
| | Phe Thr Glu Gln Tyr Lys 145 | Trp Leu Glu Ile Lys Glu Gly Lys Leu Gly 160 | |
| 15 | Cys Lys Asp Cys Ser Ala Val Arg His Leu Gly Ser Lys Ala Glu Lys 165 | | 170 175 |
| | His Val His Val Ser Lys Glu Trp Ile Ala Tyr Leu Val Thr Pro Asn 180 | | 185 190 |
| | Gly Ser Asn Lys Thr Thr Arg Gln Ala Ser Leu Arg Lys Lys Ile Arg 195 | | 200 205 |
| 20 | Glu His Asp Val Ser Lys Ala His Gly Lys Ile Gln Asp Leu Leu Lys 210 | | 215 220 |
| | Glu Ser Thr Asn Asp Ser Ile Cys Asn Leu Val His Lys Gln Asn Asn 225 | | 230 235 240 |
| 25 | Lys Asn Ile Asp Ala Thr Val Lys Val Phe Asn Thr Val Tyr Ser Leu 245 | | 250 255 |
| | Val Lys His Asn Arg Pro Leu Ser Asp Ile Glu Gly Ala Arg Glu Leu 260 | | 265 270 |
| | Gln Glu Lys Asn Gly Glu Val Asn Cys Leu Asn Thr Arg Tyr Ser Ala 275 | | 280 285 |
| 30 | Thr Arg Ile Ala Glu His Ile Ala Lys Glu Met Lys Met Lys Ile Phe 290 | | 295 300 |
| | Lys Asn Ile Ile Glu Glu Asn Ala Lys Ile Cys Ile Ile Ile Asp Glu 305 | | 310 315 320 |
| 35 | Ala Ser Thr Val Ser Lys Lys Thr Thr Leu Val Ile Tyr Leu Gln Cys 325 | | 330 335 |
| | Thr Ile Gln Ser Ala Pro Ala Pro Val Met Leu Phe Val Ala Leu Lys 340 | | 345 350 |
| | Glu Leu Val Ser Thr Ile Ala Glu Cys Ile Val Asn Thr Leu Leu Thr 355 | | 360 365 |
| 40 | Thr Leu Asn Asp Cys Gly Phe Thr Asn Glu Tyr Leu Lys Ala Asn Leu 370 | | 375 380 |
| | Ile Ala Phe Cys Ser Asp Gly Ala Asn Thr Xaa Leu Gly Arg Lys Ser 385 | | 390 395 400 |

